

File



SEQUENCE LISTING

<110> Parales, R.  
Gibson, D.  
Resnick, S.  
Lee, K.

<120> Novel naphthalene dioxygenase and methods for their use

<130> 875.006US2

<140> US 09/843,250

<141> 2001-04-26

<150> PCT/US99/25079

<151> 1999-10-26

<150> US 60/105,575

<151> 1998-10-26

<160> 65

<170> FastSEQ for Windows Version 4.0

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<211> 2265

<212> DNA

<213> Artificial Sequence

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<223> A sequence encoding an NDO mutant.

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<213> Artificial Sequence

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<223> A polypeptide encoded by SEQ ID NO:1

<400> 2

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Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
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<211> 9841

<212> DNA

<213> Artificial Sequence

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<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

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&lt;210&gt; 4

&lt;211&gt; 2515

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

&lt;400&gt; 4

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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A modified DNA molecule encoding valine at the  
 position corresponding to the F352 amino acid in  
 NDO.

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&lt;210&gt; 6

&lt;211&gt; 2294

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

<221> misc\_feature  
 <222> (186)...(186)  
 <223> n = a or t or g or c

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<400> 6
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gaggattgct ttatgacagt aaagtggatt gaagcagtcg ctctttctga catccttgaa      120
ggtgacgtcc tcggcgtgac tgtcgagggc aaggagctgg cgctgtatga agttgaaggc      180
gaaatntacg ctaccgacaa cctgtgcacg catgggtccg cccgcatgag tgatggttat      240
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aaagccctgt gcgcacccgt gacacagaac atcaaaacat atccagtcaa gattgagaac      360
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gtcttctacg ccgc                                         2294
```

<210> 7  
 <211> 4355  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A modified DNA molecule encoding valine at the  
 position corresponding to the F352 amino acid in  
 NDO.

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<400> 7
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aagccgcgct accgcgtccg ccatatgcct gagtgaagtgc gctaaggctc ggccgctcaa      180
tggcttcgag aataaagcgg gccaggtgat cttctgtcaa tctcgccgaa tgggtggaag      240
cacatcaacc tgaccggcga ttacgtctgg cggcagagcc gcagactgga ggtcgggaag      300
ttccggccgt tacggcggcc ctgaaaacct tagtgtacga ttttttccgt cttctctatt      360
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aatacatgac	tacttcagac	gattcgcagt	attcacgctg	gtgataaaca	aattcaacta	780
tgctttattg	acaaataaaa	gcacgctcac	catcatcgcg	aatacaaatc	ttataaaaaat	840
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&lt;210&gt; 8

&lt;211&gt; 2176

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

&lt;400&gt; 8

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tcgaggggcg	agaaaatcgaa	tgccccttgc	atcaaggctcg	gtttgacgtt	tgtacaggca	180
gagccctctg	cgcccccg	acagagaaca	tcaaaacata	tgagtcgaag	attgagaacc	240
tgcgcgtaat	gattgattta	agctgagaat	ttttaatagg	aggcgccccg	gaccatagag	300
cgtaattatc	cccattccat	cttttttttag	gtgaaaacat	gaattacaaa	aacaaaatct	360
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&lt;210&gt; 9

&lt;211&gt; 14462

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> A modified DNA molecule encoding valine at the

position corresponding to the F352 amino acid in  
NDO.

<400> 9

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&lt;210&gt; 11

&lt;211&gt; 15024

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

&lt;400&gt; 11

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 <212> DNA

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

&lt;400&gt; 12

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&lt;210&gt; 13

&lt;211&gt; 6779

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> A modified DNA molecule encoding valine at the position corresponding to the F352 amino acid in NDO.

&lt;400&gt; 13

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<210> 14

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:3.

<400> 14

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      20             25             30
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
      35             40             45
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
      50             55             60
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
      65             70             75             80
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
      85             90             95
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
      100            105            110
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
      115            120            125
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
      130            135            140
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
      145            150            155            160

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Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
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 Ser Gly Gly Leu Glu Leu Val Gly Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
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 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 15

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:4.

<400> 15

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 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
 20 25 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50 55 60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110

Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
 145 150 155 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 16  
 <211> 449  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:5.

<400> 16  
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln  
 1 5 10 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
 20 25 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50 55 60

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Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
65          70          75          80
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
      85          90          95
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
      100        105        110
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
      115        120        125
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
      130        135        140
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
145          150        155        160
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
      165        170        175
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
      180        185        190
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
      195        200        205
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
      210        215        220
Cys Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
225          230        235        240
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
      245        250        255
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
      260        265        270
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
      275        280        285
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
      290        295        300
Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
305          310        315        320
Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
      325        330        335
Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
      340        345        350
Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
      355        360        365
Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
      370        375        380
Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
385          390        395        400
Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
      405        410        415
Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
      420        425        430
Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
      435        440        445
Arg

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&lt;210&gt; 17

&lt;211&gt; 449

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A polypeptide encoded by SEQ ID NO:6.

&lt;400&gt; 17

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Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Phe Gly Leu Ser Gln
1          5          10          15

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Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
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 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50 55 60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
 145 150 155 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
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 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
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 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Arg Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

&lt;210&gt; 18

&lt;211&gt; 449

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A polypeptide encoded by SEQ ID NO:7.

&lt;400&gt; 18

Met	Asn	Tyr	Lys	Asn	Lys	Ile	Leu	Val	Ser	Glu	Ser	Gly	Leu	Thr	Gln	1	5	10	15
Lys	His	Leu	Ile	His	Gly	Asp	Glu	Glu	Leu	Phe	Gln	His	Glu	Leu	Arg	20	25	30	
Thr	Ile	Phe	Ala	Arg	Asn	Trp	Leu	Phe	Leu	Thr	His	Asp	Ser	Leu	Ile	35	40	45	
Pro	Ser	Pro	Gly	Asp	Tyr	Val	Thr	Ala	Lys	Met	Gly	Ile	Asp	Glu	Val	50	55	60	
Ile	Val	Ser	Arg	Gln	Ser	Asp	Gly	Ser	Ile	Arg	Ala	Phe	Leu	Asn	Val	65	70	75	80
Cys	Arg	His	Arg	Gly	Lys	Thr	Leu	Val	Asn	Ala	Glu	Ala	Gly	Asn	Ala	85	90	95	
Lys	Gly	Phe	Val	Cys	Ser	Tyr	His	Gly	Trp	Gly	Phe	Gly	Ser	Asn	Gly	100	105	110	
Glu	Leu	Gln	Ser	Val	Pro	Phe	Glu	Lys	Glu	Leu	Tyr	Gly	Glu	Ser	Leu	115	120	125	
Asn	Lys	Lys	Cys	Leu	Gly	Leu	Lys	Glu	Val	Ala	Arg	Val	Glu	Ser	Phe	130	135	140	
His	Gly	Phe	Ile	Tyr	Gly	Cys	Phe	Asp	Gln	Glu	Ala	Pro	Pro	Leu	Met	145	150	155	160
Asp	Tyr	Leu	Gly	Asp	Ala	Ala	Trp	Tyr	Leu	Glu	Pro	Ile	Phe	Lys	His	165	170	175	
Ser	Gly	Gly	Leu	Glu	Leu	Val	Gly	Pro	Pro	Gly	Lys	Val	Val	Ile	Lys	180	185	190	
Ala	Asn	Trp	Lys	Ala	Pro	Ala	Glu	Asn	Phe	Val	Gly	Asp	Ala	Tyr	His	195	200	205	
Val	Gly	Trp	Thr	His	Ala	Ser	Ser	Leu	Arg	Ser	Gly	Glu	Ser	Ile	Phe	210	215	220	
Ala	Ser	Leu	Ala	Gly	Asn	Ala	Val	Leu	Pro	Pro	Glu	Gly	Ala	Gly	Leu	225	230	235	240
Gln	Met	Thr	Ser	Lys	Tyr	Gly	Ser	Gly	Met	Gly	Val	Leu	Trp	Asp	Gly	245	250	255	
Tyr	Ser	Gly	Val	His	Ser	Ala	Asp	Leu	Val	Pro	Glu	Leu	Met	Ala	Phe	260	265	270	
Gly	Gly	Ser	Lys	Gln	Glu	Arg	Leu	Asn	Lys	Glu	Ile	Gly	Asp	Val	Arg	275	280	285	
Ala	Arg	Ile	Tyr	Arg	Ser	His	Leu	Asn	Cys	Thr	Val	Phe	Pro	Asn	Asn	290	295	300	
Ser	Met	Leu	Thr	Cys	Ser	Gly	Val	Phe	Lys	Val	Trp	Asn	Pro	Ile	Asp	305	310	315	320
Ala	Asn	Thr	Thr	Glu	Val	Trp	Thr	Tyr	Ala	Ile	Val	Glu	Lys	Asp	Met	325	330	335	
Pro	Glu	Asp	Leu	Lys	Arg	Arg	Leu	Ala	Asp	Ser	Val	Gln	Arg	Thr	Val	340	345	350	
Gly	Pro	Ala	Gly	Phe	Trp	Glu	Ser	Asp	Asp	Asn	Asp	Asn	Met	Glu	Thr	355	360	365	
Ala	Ser	Gln	Asn	Gly	Lys	Lys	Tyr	Gln	Ser	Arg	Asp	Ser	Asp	Leu	Leu	370	375	380	
Ser	Asn	Leu	Gly	Phe	Gly	Lys	Asp	Val	Tyr	Gly	Asp	Ala	Val	Tyr	Pro	385	390	395	400
Gly	Val	Val	Gly	Lys	Ser	Ala	Ile	Gly	Glu	Thr	Ser	Tyr	Arg	Gly	Phe	405	410	415	
Tyr	Arg	Ala	Tyr	Gln	Ala	His	Val	Ser	Ser	Ser	Asn	Trp	Ala	Glu	Phe	420	425	430	
Glu	Asp	Ala	Ser	Ser	Thr	Trp	His	Thr	Glu	Leu	Thr	Lys	Thr	Thr	Asp	435	440	445	

Arg

<210> 19  
 <211> 449  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A polypeptide encoded by SEQ ID NO:8.

<221> SITE  
 <222> (35)...(35)  
 <223> Xaa = any amino acid.

<400> 19  
 Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln  
 1 5 10 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Arg  
 20 25 30  
 Thr Ile Xaa Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50 55 60  
 Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Ser Leu Met  
 145 150 155 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Thr Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Pro  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Val Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Ile  
 370 375 380

Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 20

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:9.

<400> 20

Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln  
 1 5 10 15  
 Lys His Leu Ile His Gly Gly Glu Gly Leu Phe Gln His Glu Leu Arg  
 20 25 30  
 Ala Val Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50 55 60  
 Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Ala Cys Ile Asp Gln Glu Ala Pro Ser Leu Met  
 145 150 155 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Cys Thr Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Val Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335

Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Ile  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 21

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:10.

<400> 21

Met Asn Tyr Lys Asn Lys Asn Leu Val Ser Glu Ser Gly Leu Thr Gln  
 1 5 10 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln Arg Glu Leu Glu  
 20 25 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val  
 50 55 60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ala Asn Gly  
 100 105 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ala Leu  
 115 120 125  
 Asp Lys Lys Cys Met Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Glu Glu Ala Pro Ser Leu Lys  
 145 150 155 160  
 Asp Tyr Met Gly Asp Ala Gly Trp Tyr Leu Glu Pro Met Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Ile Gly Pro Gly Lys Val Ile Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Thr Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Val Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Glu Val Arg  
 275 280 285

Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Phe Leu Thr Cys Ser Gly Val Phe Lys Val Trp His Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Met Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Val Asp Ala Val Gln Arg Thr Val  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
 355 360 365  
 Val Ser Gln Asn Ala Lys Lys Tyr Gln Ser Arg Asp Gly Asp Leu Val  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Gly Asp Val Tyr Gly Asp Glu Val Tyr Pro  
 385 390 395 400  
 Gly Ile Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gly Ala His Ile Ser Ser Ser Trp Ala Glu Phe  
 420 425 430  
 Glu Asp Val Ser Lys Asn Trp His Thr Glu Leu Ala Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 22

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:11.

<400> 22

Met Ile Tyr Glu Asn Leu Val Ser Glu Ala Gly Leu Thr Gln Lys His  
 1 5 10 15  
 Leu Ile His Gly Asp Lys Glu Leu Phe Gln His Glu Leu Lys Thr Ile  
 20 25 30  
 Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser  
 35 40 45  
 Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val  
 50 55 60  
 Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg  
 65 70 75 80  
 His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala Lys Gly  
 85 90 95  
 Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly Glu Leu  
 100 105 110  
 Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Thr Ile Lys Lys  
 115 120 125  
 Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly  
 130 135 140  
 Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Thr Leu Val Asp Tyr  
 145 150 155 160  
 Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His Ser Gly  
 165 170 175  
 Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys Ala Asn  
 180 185 190  
 Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His Val Gly  
 195 200 205  
 Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Ile Phe Thr Pro  
 210 215 220  
 Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly Ala Gly Leu Gln Met  
 225 230 235 240

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Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly Tyr Ser
      245      250      255
Gly Val His Ser Ala Asp Leu Val Pro Glu Met Met Ala Phe Gly Gly
      260      265      270
Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg
      275      280      285
Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn Ser Ile
      290      295      300
Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp Glu Asn
305      310      315      320
Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met Pro Glu
      325      330      335
Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val Gly Pro
      340      345      350
Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr Glu Ser
      355      360      365
Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Leu Ile Ala Asn
      370      375      380
Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val
385      390      395      400
Val Ala Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg
      405      410      415
Ala Tyr Gln Ala His Ile Ser Ser Ser Asn Trp Ala Glu Phe Glu Asn
      420      425      430
Thr Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg
      435      440      445

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&lt;210&gt; 23

&lt;211&gt; 447

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A polypeptide encoded by SEQ ID NO:12.

&lt;400&gt; 23

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Met Ser Tyr Gln Asn Leu Val Ser Glu Ala Gly Leu Thr Gln Lys Leu
 1      5      10      15
Leu Ile His Gly Asp Lys Glu Leu Phe Gln His Glu Leu Lys Thr Ile
      20      25      30
Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser
      35      40      45
Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val
      50      55      60
Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg
65      70      75      80
His Arg Gly Lys Thr Leu Val His Thr Glu Ala Gly Asn Ala Lys Gly
      85      90      95
Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly Ser Asn Gly Glu Leu
      100      105      110
Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Ala Ile Lys Lys
      115      120      125
Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly
      130      135      140
Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Pro Leu Ile Asp Tyr
145      150      155      160
Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Thr Phe Lys His Ser Gly
      165      170      175
Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Val Lys Ala Asn
      180      185      190
Trp Lys Pro Phe Ala Glu Asn Phe Val Gly Asp Ile Tyr His Val Gly
      195      200      205

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Trp Thr His Ala Ala Ala Leu Arg Ala Gly Gln Ser Val Phe Ser Ser
 210                215                220
Leu Ala Gly Asn Ala Lys Leu Pro Pro Glu Gly Ala Gly Leu Gln Met
 225                230                235                240
Thr Ser Lys Tyr Gly Ser Gly Met Gly Leu Thr Trp Asp Tyr Tyr Ser
                245                250                255
Gly Asn Phe Ser Ala Asp Met Val Pro Asp Leu Met Ala Phe Gly Ala
 260                265                270
Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg
 275                280                285
Ile Tyr Arg Ser Ile Leu Asn Gly Thr Val Phe Pro Asn Asn Ser Phe
 290                295                300
Leu Thr Gly Ser Ala Thr Phe Lys Val Trp Asn Pro Ile Asp Glu Asn
 305                310                315                320
Thr Thr Glu Val Trp Thr Tyr Ala Phe Val Glu Lys Asp Met Pro Glu
                325                330                335
Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln Arg Ser Val Gly Pro
 340                345                350
Ala Gly Phe Trp Glu Ser Asp Asp Asn Glu Asn Met Glu Thr Leu Ser
 355                360                365
Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Gln Ile Ala Ser
 370                375                380
Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val
 385                390                395                400
Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg
                405                410                415
Ala Tyr Gln Ala His Ile Ser Ser Ser Asn Trp Ala Glu Phe Glu Asn
                420                425                430
Ala Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg
                435                440                445

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<210> 24

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:13.

<400> 24

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Met Arg Gln Ala Ile Met Ser Tyr Gln Asn Leu Val Ser Glu Ala Gly
 1                5                10                15
Leu Thr Gln Lys His Leu Ile Tyr Gly Asp Lys Glu Leu Phe Gln His
                20                25                30
Glu Leu Lys Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp
 35                40                45
Ser Leu Ile Pro Ser Pro Gly Asp Tyr Val Lys Ala Lys Met Gly Val
 50                55                60
Asp Glu Val Ile Val Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe
 65                70                75                80
Leu Asn Val Cys Arg His Arg Gly Lys Thr Ile Val Asp Ala Glu Ala
                85                90                95
Gly Asn Ala Lys Gly Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly
                100                105                110
Ser Asn Gly Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly
                115                120                125
Asp Ala Ile Lys Lys Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile
 130                135                140
Glu Ser Phe His Gly Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro
 145                150                155                160
Pro Leu Ile Asp Tyr Leu Gly Asp Val Ala Trp Tyr Leu Glu Pro Thr
                165                170                175

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Phe Lys His Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Ala Lys Val  
 180 185 190  
 Val Val Lys Gly Asn Trp Lys Val Phe Ala Glu Asn Phe Val Gly Asp  
 195 200 205  
 Ile Tyr His Ile Gly Trp Thr His Ala Ser Ile Leu Arg Ala Gly Gln  
 210 215 220  
 Ala Ile Phe Ala Pro Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly  
 225 230 235 240  
 Thr Gly Leu Gln Ala Thr Thr Lys Tyr Gly Ser Gly Ile Gly Val Ser  
 245 250 255  
 Leu Asp Ala Tyr Ser Gly Val Gln Ser Ala Asp Leu Val Pro Glu Met  
 260 265 270  
 Met Ala Phe Gly Gly Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly  
 275 280 285  
 Asp Val Arg Ala Arg Ile Tyr Arg Ser Gln Val Asn Gly Thr Val Phe  
 290 295 300  
 Pro Asn Asn Cys Phe Leu Thr Gly Ala Gly Val Phe Lys Val Phe Asn  
 305 310 315 320  
 Pro Ile Asp Glu Asn Thr Thr Glu Ala Trp Thr Tyr Ala Ile Val Glu  
 325 330 335  
 Lys Asp Met Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln  
 340 345 350  
 Arg Ser Val Gly Pro Ala Gly Tyr Trp Glu Ser Asp Asp Asn Asp Asn  
 355 360 365  
 Met Val Leu Ser Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp  
 370 375 380  
 Leu Ile Ala Asp Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys  
 385 390 395 400  
 Tyr Pro Gly Val Val Ser Lys Ser Ala Phe Ser Glu Thr Asn His Arg  
 405 410 415  
 Gly Phe Tyr Arg Ala Tyr Gln Ala His Ile Ser Ser Ser Asn Trp Ala  
 420 425 430  
 Glu Phe Glu Asn Thr Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr  
 435 440 445  
 Thr Asp Arg  
 450

&lt;210&gt; 25

&lt;211&gt; 2265

&lt;212&gt; DNA

<213> *Pseudomonas* sp.

&lt;400&gt; 25

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gccctgtg	cacccgtgac	acagaacatc	aaaacatata	cagtcagat	tgagaacctg	120
cgcgtaatga	ttgatttgag	ctaagaattt	taacaggagg	caccccgggc	cctagagcgt	180
aatcaccccc	attccatctt	ttttaggtga	aaacatgaat	tacaataata	aaatcttggt	240
aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gatgaagaac	ttttccaaca	300
tgaactgaaa	accatttttg	cgcggaactg	gctttttctc	actcatgata	gcctgattcc	360
tgcccccggc	gactatgtta	ccgcaaaaat	ggggattgac	gaggtcatcg	tctcccggca	420
gaacgacggt	tcgattcgtg	cttttctgaa	cgtttgccgg	catcgtggca	agacgctggt	480
gagcgtggaa	gccggcaatg	ccaaagggtt	tgtttgacgc	tatcacggct	ggggcttcgg	540
ctccaacggt	gaactgcaga	gcgttccatt	tgaaaaagat	ctgtacggcg	agtcgctcaa	600
taaaaaatgt	ctgggggtga	aagaagtcgc	tcgcgtggag	agcttccatg	gcttcatcta	660
cggttgcttc	gaccaggagg	cccctcctct	tatggactat	ctgggtgacg	ctgcttggtg	720
cctggaaacct	atggtccaagc	attcggcgcg	tttagaactg	gtcggtcctc	caggcaaggt	780
tgtgatcaag	gccaaactgga	aggcaccgcg	ggaaaacttt	gtgggagatg	cataccacgt	840
gggttgacg	cacgcgtctt	cgttctgcct	gggggagtc	atcttctcgt	cgctcgctgg	900
caatgcggcg	ctaccacctg	aaggcgcagg	cttgcaaatg	acctccaaat	acggcagcgg	960
catgggtgtg	ttgtgggacg	gatattcagg	tgtgcatagc	gcagacttgg	ttccggaatt	1020
gatggcattc	ggaggcgcaa	agcaggaaaag	gctgaacaaa	gaaattggcg	atgttcgcgc	1080
tcggatttat	cgcagccacc	tcaactgcac	cgttttcccg	aacaacagca	tgctgacctg	1140

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ctcgggtgtt ttcaaagtat ggaacccgat cgacgcaaac accaccgagg tctggacct 1200
cgccattgtc gaaaaagaca tgccctgagga tctcaagcgc cgcttggccg actctgttca 1260
gcgaacgttc gggcctgctg gcttctgga aagcgacgac aatgacaata tggaaacagc 1320
ttcgcaaaac ggcaagaaat atcaatcaag agatagtgat ctgctttcaa accttggttt 1380
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<210> 26

<211> 449

<212> PRT

<213> *Pseudomonas* sp.

<400> 26

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Lys His Leu Ile His Gly Asp Glu Leu Phe Gln His Glu Leu Lys
      20          25          30
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
      35          40          45
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
      50          55          60
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
      65          70          75          80
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
      85          90          95
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
      100          105          110
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
      115          120          125
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
      130          135          140
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
      145          150          155          160
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
      165          170          175
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
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Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
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Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
      245          250          255
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
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Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
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Arg

&lt;210&gt; 27

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

&lt;400&gt; 27

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&lt;210&gt; 28

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

&lt;400&gt; 28

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&lt;210&gt; 29

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

&lt;400&gt; 29

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&lt;210&gt; 30

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

&lt;400&gt; 30

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&lt;210&gt; 31

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

&lt;400&gt; 31

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ttcgcaaaac	ggcaagaaat	atcaatcaag	agatagtgat	ctgctttcaa	accttggttt	1380
cggtagggac	gtatacggcg	acgcggtcta	tccaggcgctc	gtcggcaaat	cggcgatcgg	1440

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cgagaccagt tatcgtggtt tctaccgggc ttaccaggca cacgtcagca gctccaactg 1500
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ctaacagacg agtcgaccat gatgatcaat attcaagaag acaagctggg ttccgcccac 1620
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<210> 32

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:27.

<400> 32

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Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
1      5      10      15
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
20     25     30
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
35     40     45
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
50     55     60
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
65     70     75     80
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
85     90     95
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
100    105    110
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
115    120    125
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
130    135    140
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
145    150    155    160
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
165    170    175
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
180    185    190
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
195    200    205
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
210    215    220
Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
225    230    235    240
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
245    250    255
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
260    265    270
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
275    280    285
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
290    295    300

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Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Gly  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 33

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:28.

<400> 33

Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln  
 1 5 10 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
 20 25 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50 55 60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
 145 150 155 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255

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Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
      260      265      270
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
      275      280      285
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
      290      295      300
Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
305      310      315      320
Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
      325      330      335
Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ala
      340      345      350
Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
      355      360      365
Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
      370      375      380
Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
385      390      395      400
Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
      405      410      415
Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
      420      425      430
Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
      435      440      445
Arg

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<210> 34

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:29.

<400> 34

```

Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1      5      10      15
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
      20      25      30
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
      35      40      45
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
      50      55      60
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
65      70      75      80
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
      85      90      95
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
      100      105      110
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
      115      120      125
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
      130      135      140
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
145      150      155      160
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
      165      170      175
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
      180      185      190
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
195      200      205

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Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Thr  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 35

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:30.

<400> 35

Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln  
 1 5 10 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
 20 25 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50 55 60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
 145 150 155 160

Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Leu  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 36

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:31.

<400> 36

Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln  
 1 5 10 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
 20 25 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45  
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val  
 50 55 60  
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val  
 65 70 75 80  
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala  
 85 90 95  
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110

Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
 145 150 155 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ile  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 37

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 37

ttcagcgaac ggtcgggcct gc

22

<210> 38

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> A tetracycline repair oligonucleotide.

<400> 38

gccgggcctc ttgcgggata tcgtcca

27

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> An ampicillin knockout oligonucleotide.

<400> 39

gttgccattg ctgcaggcat cgtggtg

27

<210> 40

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 40

gaggcacccg cggaagcttt tgtgggagat gca

33

<210> 41

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 41

gcacccgcgg aacaatttgt gggagatgca

30

<210> 42

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 42

ccgcggaaag ctttgtggga g

21

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> A mutagenic oligonucleotide.

<400> 43

ccgcggaaaa gcttgtggga gatg

24

<210> 44

<211> 23

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 44  
 cgcggaac gttgtgggag atg 23

<210> 45  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 45  
 atattcaggt gcgcatagcg cag 23

<210> 46  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 46  
 ggacggatat tcagggctcc atagcgaga cttg 34

<210> 47  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 47  
 gacggatatt caggtaacca tagcgagac ttg 33

<210> 48  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 48  
 ggtgttttca aagtcgcgaa cccgatcgac 30

<210> 49  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 49

ctgttcagcg aaacttcggg cctgct 26

<210> 50  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 50  
 ctgttcagcg aaggttcggg cctgct 26

<210> 51  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 51  
 ctgttcagcg aagcttcggg cctgct 26

<210> 52  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 52  
 ttcagcgaac gctcgggcct gc 22

<210> 53  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 53  
 ggctgctgg cttcgcggaagcgacgaca 30

<210> 54  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A mutagenic oligonucleotide.

<400> 54  
 gaaagcgacg ccaatgacaa t 21

<210> 55  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; A mutagenic oligonucleotide.

&lt;400&gt; 55

acgacaatga caattgggaa acagcttcgc

30

&lt;210&gt; 56

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

&lt;400&gt; 56

gagggtagag	aaatcgaatg	ccccttgc	caaggtcgg	ttgacgtttg	cacaggcaaa	60
gccctgtg	cacccgtg	acagaacat	aaaacat	cagtcaag	tgagaacctg	120
cgcgtaatga	ttgatttg	ctaagaattt	taacaggagg	caccccg	cctagagcgt	180
aatcaccccc	attccatctt	ttttagggtga	aaacatgaat	tacaataata	aaatcttggt	240
aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gatgaagaac	ttttccaaca	300
tgaactgaaa	accatttttg	cgcggaactg	gctttttctc	actcatgata	gcctgattcc	360
tgcccccg	gactatgtta	ccgcaaaaat	ggggattgac	gaggtcatcg	tctcccggca	420
gaacgacggt	tcgattcgtg	cttttctgaa	cgtttgccgg	catcgtggca	agacgctggt	480
gagcgtggaa	gccggcaatg	ccaaagggtt	tgtttgacgc	tatcacggct	ggggcttcgg	540
ctccaacggt	gaactgcaga	gcgttcatt	tgaaaaagat	ctgtacggcg	agtcgctcaa	600
taaaaaatgt	ctgggggtga	aagaagtcgc	tcgcgtggag	agcttccatg	gcttcattcta	660
cggttgcttc	gaccaggagg	cccctcctct	tatggactat	ctgggtgacg	ctgcttggtta	720
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caatgcggcg	ctaccacctg	aaggcgcagg	cttgcaaatg	acctccaaat	acggcagcgg	960
catgggtgtg	ttgtgggacg	gatattcagg	tgtgcatagc	gcagacttgg	ttccggaatt	1020
gatggcattc	ggaggcgcaa	agcaggaaag	gctgaacaaa	gaaattggcg	atgttcgcgc	1080
tcggatttat	cgcagccacc	tcaactgcac	cgttttcccg	aacaacagca	tgctgacctg	1140
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&lt;210&gt; 57

&lt;211&gt; 2265

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A sequence encoding an NDO mutant.

&lt;400&gt; 57

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&lt;210&gt; 58

&lt;211&gt; 449

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A polypeptide encoded by SEQ ID NO:56.

&lt;400&gt; 58

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Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1             5             10             15
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20             25             30
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35             40             45
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50             55             60
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65             70             75             80
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85             90             95

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Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly  
 100 105 110  
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu  
 115 120 125  
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe  
 130 135 140  
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met  
 145 150 155 160  
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His  
 165 170 175  
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys  
 180 185 190  
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His  
 195 200 205  
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe  
 210 215 220  
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu  
 225 230 235 240  
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly  
 245 250 255  
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe  
 260 265 270  
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg  
 275 280 285  
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn  
 290 295 300  
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp  
 305 310 315 320  
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met  
 325 330 335  
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Trp  
 340 345 350  
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr  
 355 360 365  
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu  
 370 375 380  
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro  
 385 390 395 400  
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe  
 405 410 415  
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe  
 420 425 430  
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp  
 435 440 445  
 Arg

<210> 59

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:57.

<400> 59

Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln  
 1 5 10 15  
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys  
 20 25 30  
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile  
 35 40 45

Pro	Ala	Pro	Gly	Asp	Tyr	Val	Thr	Ala	Lys	Met	Gly	Ile	Asp	Glu	Val
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Ile	Val	Ser	Arg	Gln	Asn	Asp	Gly	Ser	Ile	Arg	Ala	Phe	Leu	Asn	Val
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Cys	Arg	His	Arg	Gly	Lys	Thr	Leu	Val	Ser	Val	Glu	Ala	Gly	Asn	Ala
				85					90					95	
Lys	Gly	Phe	Val	Cys	Ser	Tyr	His	Gly	Trp	Gly	Phe	Gly	Ser	Asn	Gly
			100					105					110		
Glu	Leu	Gln	Ser	Val	Pro	Phe	Glu	Lys	Asp	Leu	Tyr	Gly	Glu	Ser	Leu
		115					120					125			
Asn	Lys	Lys	Cys	Leu	Gly	Leu	Lys	Glu	Val	Ala	Arg	Val	Glu	Ser	Phe
	130					135				140					
His	Gly	Phe	Ile	Tyr	Gly	Cys	Phe	Asp	Gln	Glu	Ala	Pro	Pro	Leu	Met
145					150				155					160	
Asp	Tyr	Leu	Gly	Asp	Ala	Ala	Trp	Tyr	Leu	Glu	Pro	Met	Phe	Lys	His
				165					170					175	
Ser	Gly	Gly	Leu	Glu	Leu	Val	Gly	Pro	Gly	Lys	Val	Val	Ile	Lys	
			180					185					190		
Ala	Asn	Trp	Lys	Ala	Pro	Ala	Glu	Asn	Phe	Val	Gly	Asp	Ala	Tyr	His
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	210					215					220				
Ser	Ser	Leu	Ala	Gly	Asn	Ala	Ala	Leu	Pro	Pro	Glu	Gly	Ala	Gly	Leu
225					230				235					240	
Gln	Met	Thr	Ser	Lys	Tyr	Gly	Ser	Gly	Met	Gly	Val	Leu	Trp	Asp	Gly
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Tyr	Ser	Gly	Val	His	Ser	Ala	Asp	Leu	Val	Pro	Glu	Leu	Met	Ala	Phe
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Gly	Gly	Ala	Lys	Gln	Glu	Arg	Leu	Asn	Lys	Glu	Ile	Gly	Asp	Val	Arg
		275					280					285			
Ala	Arg	Ile	Tyr	Arg	Ser	His	Leu	Asn	Cys	Thr	Val	Phe	Pro	Asn	Asn
	290					295				300					
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				325					330					335	
Pro	Glu	Asp	Leu	Lys	Arg	Arg	Leu	Ala	Asp	Ser	Val	Gln	Arg	Thr	Tyr
			340					345					350		
Gly	Pro	Ala	Gly	Phe	Trp	Glu	Ser	Asp	Asp	Asn	Asp	Asn	Met	Glu	Thr
		355					360					365			
Ala	Ser	Gln	Asn	Gly	Lys	Lys	Tyr	Gln	Ser	Arg	Asp	Ser	Asp	Leu	Leu
	370					375					380				
Ser	Asn	Leu	Gly	Phe	Gly	Glu	Asp	Val	Tyr	Gly	Asp	Ala	Val	Tyr	Pro
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Gly	Val	Val	Gly	Lys	Ser	Ala	Ile	Gly	Glu	Thr	Ser	Tyr	Arg	Gly	Phe
				405					410					415	
Tyr	Arg	Ala	Tyr	Gln	Ala	His	Val	Ser	Ser	Asn	Trp	Ala	Glu	Phe	
			420					425				430			
Glu	His	Ala	Ser	Ser	Thr	Trp	His	Thr	Glu	Leu	Thr	Lys	Thr	Thr	Asp
		435					440					445			

Arg

&lt;210&gt; 60

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; A mutagenic oligonucleotide.

&lt;400&gt; 60

gttcagcgaa cgggcggggcc tgctgg 26

<210> 61  
 <211> 26  
 <212> DNA  
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